

1 GAATATGATG ACCCTAATGC AACAAATATCT AACATACTAT CCGAGCTTCG
51 GTCATTTGGA AGAACTGCAG ATTTTCCTCC TTCAAATAA AAGTCAGGTT
101 ATGGAGAACA TGTATGCTAT GTTCTTGATT GCTTCGCTGA AGAAGCATTG
151 AAATATATTG GTTTCACCTG GAAAAGGCCA ATATACCCAG TAGAAGAATT
201 AGAAGAAGAA AGCGTTGCAG AAGATGATGC AGAATTAACA TTAAATAAAG
251 TGGATGAAGA ATTTGTGGAA GAAGAGACAG ATAATGAAGA AAACCTTTATT
301 GATCTCAACG TTTTAAAGGC CCAGACATAT CACTTGGATA TGAACGAGAC
351 TGCCAAACAA GAAGATATTT TGGAAATCCAC AACAGATGCT GCAGAATGGA
401 GCCTAGAAGT GGAACGTGTA CTACCGCAAC TGAAAGTCAC GATTAGGACT
451 GACAATAAGG ATTGGAGAAT CCATGTTGAC CAAATGCACC AGCACAGAAG
501 TGGAAATTGAA TCTGCTCTAA AGGAGACCAA GGGATTTTTG GACAACTCC
551 ATAATGAAAT TACTAGGACT TTGGAAAAGA TCAGCAGCCG AGAAAAGTAC
601 ATCAACAATC AGCCGGGAGC CCATGGAGCA CTGTCCTCAG AGATGCGCAG
651 GTTAGGCTCA CTGTCTAGGC CAGGCCACACC TTAGTCACTG TGGACTGGCA
701 ATGGAAGCTC TTCCTGGACA CACCTGCCCT AGCCCTCACC CTGGGGTGGA
751 AGAGAAATGA GCTTGGCTTG CAACTCAGAC CATTCCACGG AGGCATCCTC
801 CCCTTCCCTG GGCTGGTGAA TAAAAGTTTC CTGAGGTCAA GGAATTCCTT
851 TTCCCTGCCA AAATGGTGTC CAGAACTTTG AGGCCAGAGG TGATCCAGTG

FIG.1A

901 ATTTGGGAGC TGCAGGTCAC ACAGGCTGCT CAGAGGGCTG CTGAACAGGA
951 TGTCTCGGA CGACAGGCAC CTGGGCTCCA GCTGCGGCTC CTTCATCAAG
1001 ACTGAGCCGT CCAGCCCGTC CTCGGGCATA GATGCCCTCA GCCACCACAG
1051 CCCAGTGGC TCGTCCGACG CCAGCGGCGG CTTTGGCCTG GCCCTGGGCA
1101 CCCACGCCAA CGGTCTGGAC TCGCCACCCA TGTTTGCAGG CGCCGGGCTG
1151 GGAGGCACCC CATGCCGCAA GAGCTACGAG GACTGTGCCA GCGGCATCAT
1201 GGAGGACTCG GCCATCAAGT GCGAGTACAT GCTCAACGCC ATCCCAAGC
1251 GCCTGTGCCT CGTGTGCGGG GACATTGCCT CTGGCTACCA CTACGGCGTG
1301 GCCTCCTGCG AGGCTTGCAA GGCCTTCTTC AAGAGGACTA TCCAAGGGAA
1351 CATTGAGTAC AGCTGCCCGG CCACCAACGA GTGCGAGATC ACCAAACGGA
1401 GGCGCAAGTC CTGCCAGGCC TGCCGCTTCA TGAAATGCCT CAAAGTGGGG
1451 ATGCTGAAGG AAGGTGTGCG CCTTGATCGA GTGCGTGGAG GCCGTCAGAA
1501 ATACAAGCGA CGGCTGGACT CAGAGAGCAG CCCATACCTG AGCTTACAAA
1551 TTTCTCCACC TGCTAAAAAG CCATTGACCA AGATTGTCTC ATACCTACTG
1601 GTGGCTGAGC CGGACAAGCT CTATGCCATG CCTCCCCCTG GTATGCCTGA
1651 GGGGGACATC AAGGCCCTGA CCACTCTCTG TGACCTGGCA GACCGAGAGC
1701 TTGTGGTCAT CATTGGCTGG GCCAAGCACA TCCAGGCTT CTCAAGCCTC
1751 TCCCTGGGGG ACCAGATGAG CCTGCTGCAG AGTGCCTGGA TGGAAATCCT

FIG.1B

1801 CATCCTGGGC ATCGTGTACC GCTCGCTGCC CTACGACGAC AAGCTGGTGT
1851 ACGCTGAGGA CTACATCATG GATGAGGAGC ACTCCCGCCT CGCGGGGCTG
1901 CTGGAGCTCT ACCGGGCCAT CCTGCAGCTG GTACGCAGGT ACAAGAAGCT
1951 CAAGGTGGAG AAGGAGGAGT TTGTGACGCT CAAGGCCCTG GCCCTCGCCA
2001 ACTCCGATTC CATGTACATC GAGGATCTAG AGGCTGTCCA GAAGCTGCAG
2051 GACCTGCTGC ACGAGGCACT GCAGGACTAC GAGCTGAGCC AGCGCCATGA
2101 GGAGCCCTGG AGGACGGGCA AGCTGCTGCT GACACTGCCG CTGCTGCGGC
2151 AGACGGCCGC CAAGGCCGTG CAGCACTTCT ATAGCGTCAA ACTGCAGGGC
2201 AAAGTGCCCA TGCACAACT CTTCCTGGAG ATGCTGGAGG CCAAGGCCTG
2251 GGCCAGGGCT GACTCCCTTC AGGAGTGGAG GCCACTGGAG CAAGTGCCCT
2301 CTCCCCTCCA CCGAGCCACC AAGAGGCAGC ATGTGCATTT CCTAACTCCC
2351 TTGCCCCCTC CCCCATCTGT GGCCTGGGTG GGCAGTCTC AGGCTGGATA
2401 CCACCTGGAG GTTTTCCTTC CGCAGAGGGC AGGTTGGCCA AGAGCAGCTT
2451 AGAGGATCTC CCAAGGATGA AAGAATGTCA AGCCATGATG GAAAATGCCC
2501 CTTCCAATCA GCTGCCTTCA CAAGCAGGGA TCAGAGCAAC TCCCCGGGGA
2551 TCCCCAATCC ACGCCCTTCT AGTCCAACCC CCCTCAATGA GAGAGGCAGG
2601 CAGATCTCAC CCAGCACTAG GACACCAGGA GGCCAGGGAA AGCATCTCTG
2651 GCTCACCATG TAACATCTGG CTTGGAGCAA GTGGGTGTTC TGCACACCAG
2701 GCAGCTGCAC CTCACTGGAT CTAGTGTTGC TGCGAGTGAC CTCACTTCAG
2751 AGCCCCTCTA GCAGAGTGGG GCGGAAGTCC TGATGGTTGG TGTCCATGAG
2801 GTGGAAG (SEQ.ID NO:1)

FIG.1C

4/26

GAATATGATGACCCTAATGCAACAATATCTAACATACTATCCGAGCTTCGGTCATTTGGA
1 -----+-----+-----+-----+-----+-----+ 60
CTTATACTACTGGGATTACGTTGTTATAGATTGTATGATAGGCTCGAAGCCAGTAAACCT

AGAACTGCAGATTTTCCTCCTTCAAATTAAGTCAGGTTATGGAGAACATGTATGCTAT
61 -----+-----+-----+-----+-----+-----+ 120
TCTTGACGTCTAAAAGGAGGAAGTTTAAATTTAGTCCAATACCTCTTGTACATACGATA

GTTCTTGATTGCTTCGCTGAAGAAGCATTGAAATATATTGGTTTCACCTGGAAAAGGCCA
121 -----+-----+-----+-----+-----+-----+ 180
CAAGAACTAACGAAGCGACTTCTTCGTAACCTTATATAACCAAAGTGGACCTTTTCCGGT

ATATACCCAGTAGAAGAATTAGAAGAAGAAAGCGTTGCAGAAGATGATGCAGAATTAACA
181 -----+-----+-----+-----+-----+-----+ 240
TATATGGGTCATCTTCTTAATCTTCTTCTTCGCAACGTCTTCTACTACGTCTTAATTGT

TTAAATAAAGTGGATGAAGAATTTGTGGAAGAAGAGACAGATAATGAAGAAAACCTTTATT
241 -----+-----+-----+-----+-----+-----+ 300
AATTTATTTACCTACTTCTTAACACCTTCTTCTGTCTATTACTTCTTTTGAAATAA

GATCTCAACGTTTTAAAGGCCAGACATATCACTTGGATATGAACGAGACTGCCAAACAA
301 -----+-----+-----+-----+-----+-----+ 360
CTAGAGTTGCAAATTTCCGGGTCTGTATAGTGAACCTATACTTGCTCTGACGGTTTGTT

GAAGATATTTTGAATCCACAACAGATGCTGCAGAATGGAGCCTAGAAGTGGAACGTGTA
361 -----+-----+-----+-----+-----+-----+ 420
CTTCTATAAAACCTTAGGTGTTGTCTACGACGTCTTACCTCGGATCTTACCTTGACAT

CTACCGCAACTGAAAGTCACGATTAGGACTGACAATAAGGATTGGAGAATCCATGTTGAC
421 -----+-----+-----+-----+-----+-----+ 480
GATGGCGTTGACTTTAGTGCTAATCCTGACTGTTATTCCTAACCTCTTAGGTACAACCTG

CAAATGCACCAGCACAGAAGTGAATTGAATCTGCTCTAAAGGAGACCAAGGGATTTTTG
481 -----+-----+-----+-----+-----+-----+ 540
GTTTACGTGGTCGTGTCTTACCTTAACCTTAGACGAGATTTCTCTGGTTCCCTAAAAAC

FIG.2A

1054941.041602

5/26

541 GACAAACTCCATAATGAAATTACTAGGACTTTGGAAAAGATCAGCAGCCGAGAAAAGTAC 600
 -----+-----+-----+-----+-----+-----+-----+
 CTGTTTGAGGTATTACTTTAATGATCCTGAAACCTTTTCTAGTCGTCGGCTCTTTTCATG

 601 ATCAACAATCAGCCGGGAGCCCATGGAGCACTGTCCTCAGAGATGCGCAGGTTAGGCTCA 660
 -----+-----+-----+-----+-----+-----+-----+
 TAGTTGTTAGTCGGCCCTCGGGTACCTCGTGACAGGAGTCTCTACGCGTCCAATCCGAGT

 661 CTGTCTAGGCCAGGCCACCTTAGTCACTGTGGACTGGCAATGGAAGCTCTTCCTGGACA 720
 -----+-----+-----+-----+-----+-----+-----+
 GACAGATCCGGTCCGGGTGGAATCAGTGACACCTGACCGTTACCTTCGAGAAGGACCTGT

 721 CACCTGCCCTAGCCCTCACCTGGGGTGGGAAGAGAAATGAGCTTGGCTTGCAACTCAGAC 780
 -----+-----+-----+-----+-----+-----+-----+
 GTGGACGGGATCGGGAGTGGGACCCACCTTCTCTTTACTCGAACCGAACGTTGAGTCTG

 781 CATTCCACGGAGGCATCCTCCCCTTCCCTGGGCTGGTGAATAAAAGTTTCCTGAGGTCAA 840
 -----+-----+-----+-----+-----+-----+-----+
 GTAAGGTGCCTCCGTAGGAGGGGAAGGGACCCGACCACTTATTTTCAAAGGACTCCAGTT

 841 GGACTTCCTTTTCCCTGCCAAAATGGTGTCCAGAACTTTGAGGCCAGAGGTGATCCAGTG 900
 -----+-----+-----+-----+-----+-----+-----+
 CCTGAAGGAAAAGGGACGGTTTTACCACAGGTCTTGAAACTCCGGTCTCCACTAGGTCAC

 901 ATTTGGGAGCTGCAGGTCACACAGGCTGCTCAGAGGGCTGCTGAACAGGATGTCCTCGGA 960
 -----+-----+-----+-----+-----+-----+-----+
 TAAACCCTCGACGTCCAGTGTGTCCGACGAGTCTCCCGACGACTTGTCCTACAGGAGCCT
 M S S D

 961 CGACAGGCACCTGGGCTCCAGCTGCGGCTCCTTCATCAAGACTGAGCCGTCCAGCCCGTC 1020
 -----+-----+-----+-----+-----+-----+-----+
 GCTGTCCGTGGACCCGAGGTCGACGCCGAGGAAGTAGTTCTGACTCGGCAGGTCCGGGCAG
 D R H L G S S C G S F I K T E P S S P S

FIG.2B

10054841.041602

6/26

CTCGGGCATAGATGCCCTCAGCCACCACAGCCCCAGTGGCTCGTCCGACGCCAGCGGGCGG
1021 -----+-----+-----+-----+-----+-----+ 1080
GAGCCCGTATCTACGGGAGTCGGTGGTGTGCGGGTCACCGAGCAGGCTGCGGTGCGCGCC
S G I D A L S H H S P S G S S D A S G G

CTTTGGCCTGGCCCTGGGCACCCACGCCAACGGTCTGGACTCGCCACCCATGTTTGCAGG
1081 -----+-----+-----+-----+-----+-----+ 1140
GAAACCGGACCGGGACCCGTGGGTGCGGTGCCAGACCTGAGCGGTGGGTACAAACGTCC
F G L A L G T H A N G L D S P P M F A G

CGCCGGGCTGGGAGGCACCCCATGCCGCAAGAGCTACGAGGACTGTGCCAGCGGCATCAT
1141 -----+-----+-----+-----+-----+-----+ 1200
GCGGCCCCGACCCTCCGTGGGGTACGGCGTTCTCGATGCTCCTGACACGGTCGCCGTAGTA
A G L G G T P C R K S Y E D C A S G I M

GGAGGACTCGGCCATCAAGTGCGAGTACATGCTCAACGCCATCCCCAAGCGCCTGTGCCT
1201 -----+-----+-----+-----+-----+-----+ 1260
CCTCCTGAGCCGGTAGTTACGCTCATGTACGAGTTGCGGTAGGGGTTGCGGACACGGA
E D S A I K C E Y M L N A I P K R L C L

CGTGTGCGGGGACATTGCCTCTGGCTACCACTACGGCGTGGCCTCCTGCGAGGCTTGCAA
1261 -----+-----+-----+-----+-----+-----+ 1320
GCACACGCCCCTGTAACGGAGACCGATGGTGATGCCGCACCGGAGGACGCTCCGAACGTT
V C G D I A S G Y H Y G V A S C E A C K

GGCCTTCTTCAAGAGGACTATCCAAGGGAACATTGAGTACAGCTGCCCGGCCACCAACGA
1321 -----+-----+-----+-----+-----+-----+ 1380
CCGGAAGAAGTTCTCCTGATCGGTTCCCTTGTAACCTCATGTGACGGGCGGTGGTTGCT
A F F K R T I Q G N I E Y S C P A T N E

GTGCGAGATCACCAAACGGAGGCGCAAGTCCTGCCAGGCCTGCCGCTTCATGAAATGCCT
1381 -----+-----+-----+-----+-----+-----+ 1440
CACGCTCTAGTGGTTTGCCTCCGCGTTCAGGACGGTCCGGACGGCGAAGTACTTTACGGA
C E I T K R R R K S C Q A C R F M K C L

FIG.2C

10064641-041602

7/26

CAAAGTGGGGATGCTGAAGGAAGGTGTGCGCCTTGATCGAGTGCGTGGAGGCCGTCAGAA
1441 -----+-----+-----+-----+-----+-----+ 1500
GTTTCACCCCTACGACTTCCTTCCACACGCGGAAGTAGCTCACGCACCTCCGGCAGTCTT
 K V G M L K E G V R L D R V R G G R Q K

ATACAAGCGACGGCTGGACTCAGAGAGCAGCCCATACCTGAGCTTACAAATTTCTCCACC
1501 -----+-----+-----+-----+-----+-----+ 1560
TATGTTGCTGCCGACCTGAGTCTCTCGTCGGGTATGGACTCGAATGTTTAAAGAGGTGG
 Y K R R L D S E S S P Y L S L Q I S P P

TGCTAAAAAGCCATTGACCAAGATTGTCTCATACCTACTGGTGGCTGAGCCGGACAAGCT
1561 -----+-----+-----+-----+-----+-----+ 1620
ACGATTTTTTCGGTAACTGGTTCTAACAGAGTATGGATGACCACCGACTCGGCCTGTTTGA
 A K K P L T K I V S Y L L V A E P D K L

CTATGCCATGCCTCCCCCTGGTATGCCTGAGGGGGACATCAAGGCCCTGACCACTCTCTG
1621 -----+-----+-----+-----+-----+-----+ 1680
GATACGGTACGGAGGGGGACCATACGGAAGTCCCCCTGTAGTTCCGGGACTGGTGAGAGAC
 Y A M P P P G M P E G D I K A L T T L C

TGACCTGGCAGACCGAGAGCTTGTGGTCATCATTGGCTGGGCCAAGCACATCCCAGGCTT
1681 -----+-----+-----+-----+-----+-----+ 1740
ACTGGACCGTCTGGCTCTCGAACACCAGTAGTAACCGACCCGGTTCGTGTAGGGTCCGAA
 D L A D R E L V V I I G W A K H I P G F

CTCAAGCCTCTCCCTGGGGGACCAGATGAGCCTGCTGCAGAGTGCCTGGATGGAAATCCT
1741 -----+-----+-----+-----+-----+-----+ 1800
GAGTTCGGAGAGGGGACCCCCTGGTCTACTCGGACGACGTCTCACGGACCTACCTTTAGGA
 S S L S L G D Q M S L L Q S A W M E I L

CATCCTGGGCATCGTGTACCGCTCGCTGCCCTACGACGACAAGCTGGTGTACGCTGAGGA
1801 -----+-----+-----+-----+-----+-----+ 1860
GTAGGACCCGTAGCACATGGCGAGCGACGGGATGCTGCTGTTTCGACCACATGCGACTCCT
 I L G I V Y R S L P Y D D K L V Y A E D

FIG.2D

8/26

CTACATCATGGATGAGGAGCACTCCCGCCTCGCGGGGCTGCTGGAGCTCTACCGGGCCAT
1861 -----+-----+-----+-----+-----+-----+ 1920
GATGTAGTACCTACTCCTCGTGAGGGCGGAGCGCCCCGACGACCTCGAGATGGCCCGGTA
Y I M D E E H S R L A G L L E L Y R A I

CCTGCAGCTGGTACGCAGGTACAAGAAGCTCAAGGTGGAGAAGGAGGAGTTTGTGACGCT
1921 -----+-----+-----+-----+-----+-----+ 1980
GGACGTCGACCATGCGTCCATGTTCTTCGAGTTCCACCTCTTCCTCCTCAAACACTGCGA
L Q L V R R Y K K L K V E K E E F V T L

CAAGGCCCTGGCCCTCGCCAACTCCGATTCCATGTACATCGAGGATCTAGAGGCTGTCCA
1981 -----+-----+-----+-----+-----+-----+ 2040
GTTCCGGGACCGGGAGCGGTTGAGGCTAAGGTACATGTAGCTCCTAGATCTCCGACAGGT
K A L A L A N S D S M Y I E D L E A V Q

GAAGCTGCAGGACCTGCTGCACGAGGCACTGCAGGACTACGAGCTGAGCCAGCGCCATGA
2041 -----+-----+-----+-----+-----+-----+ 2100
CTTCGACGTCCTGGACGACGTGCTCCGTGACGTCCTGATGCTCGACTCGGTTCGCGGTACT
K L Q D L L H E A L Q D Y E L S Q R H E

GGAGCCCTGGAGGACGGGCAAGCTGCTGCTGACACTGCCGCTGCTGCGGCAGACGGCCGC
2101 -----+-----+-----+-----+-----+-----+ 2160
CCTCGGGACCTCCTGCCCCGTTTCGACGACGACTGTGACGGCGACGACGCCGTCTGCCGGCG
E P W R T G K L L L T L P L L R Q T A A

CAAGGCCGTGCAGCACTTCTATAGCGTCAAAGTGCAGGGCAAAGTGCCCATGCACAACT
2161 -----+-----+-----+-----+-----+-----+ 2220
GTTCCGGCACGTCGTGAAGATATCGCAGTTTGACGTCCCGTTTCACGGGTACGTGTTTGA
K A V Q H F Y S V K L Q G K V P M H K L

CTTCCTGGAGATGCTGGAGGCCAAGGCCTGGGCCAGGGCTGACTCCCTTCAGGAGTGGAG
2221 -----+-----+-----+-----+-----+-----+ 2280
GAAGGACCTCTACGACCTCCGGTTCCGGACCCGGTCCCGACTGAGGGAAGTCCTCACCTC
F L E M L E A K A W A R A D S L Q E W R

FIG.2E

1054841.041602

9/26

2281 GCCACTGGAGCAAGTGCCCTCTCCCCTCCACCGAGCCACCAAGAGGCAGCATGTGCATTT
 -----+-----+-----+-----+-----+-----+ 2340
 CGGTGACCTCGTTCACGGGAGAGGGGAGGTGGCTCGGTGGTTCTCCGTCGTACACGTAAA
 P L E Q V P S P L H R A T K R Q H V H F

 2341 CCTAACTCCCTTGCCCCCTCCCCATCTGTGGCCTGGGTGGGCACTGCTCAGGCTGGATA
 -----+-----+-----+-----+-----+-----+ 2400
 GGATTGAGGGAACGGGGGAGGGGGTAGACACCGGACCCACCCGTGACGAGTCCGACCTAT
 L T P L P P P P S V A W V G T A Q A G Y

 2401 CCACCTGGAGGTTTTCTTCCGCAGAGGGCAGGTTGGCCAAGAGCAGCTTAGAGGATCTC
 -----+-----+-----+-----+-----+-----+ 2460
 GGTGGACCTCCAAAAGGAAGGCGTCTCCCGTCCAACCGGTTCTCGTCGAATCTCCTAGAG
 H L E V F L P Q R A G W P R A A * (SEQ ID NO:2)

 2461 CCAAGGATGAAAGAATGTCAAGCCATGATGGAAAATGCCCCTTCCAATCAGCTGCCTTCA
 -----+-----+-----+-----+-----+-----+ 2520
 GGTTCTACTTTCTTACAGTTCGGTACTACCTTTTACGGGGAAGGTTAGTCGACGGAAGT

 2521 CAAGCAGGGATCAGAGCAACTCCCCGGGGATCCCCAATCCACGCCCTTCTAGTCCAACCC
 -----+-----+-----+-----+-----+-----+ 2580
 GTTCGTCCCTAGTCTCGTTGAGGGGCCCTAGGGGTTAGGTGCGGGAAGATCAGGTTGGG

 2581 CCCTCAATGAGAGAGGCAGGCAGATCTCACCCAGCACTAGGACACCAGGAGGCCAGGGAA
 -----+-----+-----+-----+-----+-----+ 2640
 GGGAGTTACTCTCTCCGTCCGTCTAGAGTGGGTGCTGATCCTGTGGTCCTCCGGTCCCTT

 2641 AGCATCTCTGGCTCACCATGTAACATCTGGCTTGGAGCAAGTGGGTGTTCTGCACACCAG
 -----+-----+-----+-----+-----+-----+ 2700
 TCGTAGAGACCGAGTGGTACATTGTAGACCGAACCTCGTTCACCCACAAGACGTGTGGTC

 2701 GCAGCTGCACCTCACTGGATCTAGTGTTGCTGCGAGTGACCTCACTTCAGAGCCCCTCTA
 -----+-----+-----+-----+-----+-----+ 2760
 CGTCGACGTGGAGTGACCTAGATCACAACGACGCTCACTGGAGTGAAGTCTCGGGGAGAT

 2761 GCAGAGTGGGGCGGAAGTCCTGATGGTTGGTGTCCATGAGGTGGAAG (SEQ ID NO:1)
 -----+-----+-----+-----+-----+ 2807
 CGTCTCACCCCGCCTTCAGGACTACCAACCACAGGTACTCCACCTTC (SEQ ID NO:29)

FIG.2F

10/26

MSSDDRHLGS SCGSFIKTEP SSPSSGIDAL SHHSPSGSSD ASGGFGLALG
THANGLDSPP MFAGAGLGGT PCRKSYEDCA SGIMEDSAIK CEYMLNAIPK
RLCLVCGDIA SGYHYGVASC EACKAFFKPT IOGNIEYSCP ATNICEITKR
RRKSCOACRF MKCLKVGMLK EGVRLDRVRG GRQKYKRRLD SESSPYLSLQ
ISPPAKKPLT KIVSYLLVAE PDKLYAMPPP GMPRGDIKAL TTLCDLADRE
LVVIIGWAKH IPGFSSLSLG DQMSLLQSAW MEILILGIVY RSLPYDDKLV
YAEDYIMDEE HSRLAGLLEL YRAILQLVRR YKKLKVEKEE FVTLKALALA
NSDSMYIEDL EAVQKLQDLL HEALQDYELS QRHEEPWRTG KLLLTPLLR
QTAAKAVQHF YSVKLQGKVP MHKLFLEMLE AKAWARADSL QEWRPLEQVP
SPLHRATKRQ HVHFLTPLPP PPSVAWVGTA QAGYHLEVFL PQRAGWPRAA
(SEQ ID NO:2)

FIG.3

10064841.041602

11/26

1 GCGGGCCGCC AGTGTGGTGG AATTCGGCTT GTCACTAGGA ??????????
51 GTTAATTGCA CTGTGCTCTG TCAAGGAAAC TTTGATTTAT AGCTGGGGTG
101 CACAAATAAT GGTGCGCGGT CGCACATGGA TTCGGTAGAA CTTTGCCTTC
151 CTGAATCTTT TTCCCTGCAC TACGAGGAAG AGCTTCTCTG CAGAATGTCA
201 AACAAAGATC GACACATTGA TTCCAGCTGT TCGTCCTTCA TCAAGACGGA
251 ACCTTCCAGC CCAGCCTCCC TGACGGACAG CGTCAACCAC CACAGCCCTG
301 GTGGCTCTTC AGACGCCAGT GGGAGCTACA GTTCAACCAT GAATGGCCAT
351 CAGAACGGAC TTGACTCGCC ACCTCTCTAC CCTTCTGCTC CTATCCTGGG
401 AGGTAGTGGG CCTGTCAGGA AACTGTATGA TGA CTGCTCC AGCACCATTG
451 TTGAAGATCC CCAGACCAAG TGTGAATACA TGCTCAACTC GATGCCCAAG
501 AGACTGTGTT TAGTGTGTGG TGACATCGCT TCTGGGTACC ACTATGGGGT
551 AGCATCATGT GAAGCCTGCA AGGCATTCTT CAAGAGGACA ATTCAAGGCA
601 ATATAGAATA CAGCTGCCCT GCCACGAATG AATGTGAAAT CACAAAGCGC
651 AGACGTAAAT CCTGCCAGGC TTGCCGCTTC ATGAAGTGTT TAAAAGTGGG
701 CATGCTGAAA GAAGGGGTGC GTCTTGACAG AGTACGTGGA GGTCGGCAGA
751 AGTACAAGCG CAGGATAGAT GCGGAGAACA GCCCATACCT GAACCCTCAG
801 CTGGTTCAGC CAGCCAAAAA GCCATATAAC AAGATTGTCT CACATTTGTT
851 GGTGGCTGAA CCGGAGAAGA TCTATGCCAT GCCTGACCCT ACTGTCCCCG
901 ACAGTGACAT CAAAGCCCTC ACTACAGTGT GTGACTTGGC CGACCGAGAG
951 TTGGTGGTTA TCATTGGATG GGCGAAGCAT ATTCCAGGCT TCTCCACGCT
1001 GTCCCTGGCG GACCAGATGA GCCTTCTGCA GAGTGCTTGG ATGGAAATTT
1051 TGATCCTTGG TGTCGTATAC CGGTCTCTTT CATTTGAGGA TGA ACTTGTC

FIG.4A

1054941.041609

12/26

1101 TATGCAGACG ATTATATAAT GGACGAAGAC CAGTCCAAAT TAGCAGGCCT
1151 TCTTGATCTA AATAATGCTA TCCTGCAGCT GGTAAGAGAAA TACAAGAGCA
1201 TGAAGCTGGA AAAAGAAGAA TTTGTCACCC TCAAAGCTAT AGCTCTTGCT
1251 AATTCAGACT CCATGCACAT AGAAGATGTT GAAGCCGTTC AGAAGCTTCA
1301 GGATGTCTTA CATGAAGCGC TGCAGGATTA TGAAGCTGGC CAGCACATGG
1351 AAGACCCTCG TCGAGCTGGC AAGATGCTGA TGACACTGCC ACTCCTGAGG
1401 CAGACCTCTA CCAAGGCCGT GCAGCATTTC TACAACATCA AACTAGAAGG
1451 CAAAGTCCCA ATGCACAAAC TTTTTTTGGA AATGTTGGAG GCCAAGGTCT
1501 GACTAAAAGC TCCCTGGGCC TTCCCATCCT TCATGTTGAA AAAGGGAAAA
1551 TAAACCCAAG AGTGATGTCG AAGAACTTA GAGTTTAGTT AACAACATCA
1601 AAAATCAACA GACTGCACTG ATAATTTAGC AGCAAGACTA TGAAGCAGCT
1651 TTCAGATTCC TCCATAGGTT CCTGATGAGT TCTTTCTACT TTCTCCATCA
1701 TCTTCTTTCC TCTTTCTTCC CACATTTCTC TTTCTCTTA TTTTTTCTCC
1751 TTTTCTTCTT TCACCTCCCT TATTTCTTTG CTTCTTTCAT TCCTAGTTCC
1801 CATTCTCCTT TATTTTCTTC CCGTCTGCCT GCCTTCTTTC TTTTCTTTAC
1851 CTACTCTCAT TCCTCTCTTT TCTCATCCTT CCCCTTTTTT CTAAATTTGA
1901 AATAGCTTTA GTTTAAAAAA AAAAATCCTC CCTTCCCCCT TTCCTTTCCC
1951 TTTCTTTCCT TTTTCCCTTT CCTTTTCCCT TTCCTTTCCT TTCCTCTTGA
2001 CCTTCTTTCC ATCTTTCTTT TTCTTCCTTC TGCTGCTGAA CTTTAAAAG
2051 AGGTCTCTAA GTGAAGAGAG ATGGAAGCCA GCCCTGCCAA AGGATGGAGA
2101 TCCATAATAT GGATGCCAGT GAACTTATTG TGAACCATAC CGTCCCCAAT
2151 GACTAAGGAA TCAAAGAGAG AGAACCAACG TTCCTAAAAG TACAGTGCAA
2201 CATATACAAA TTGACTGAGT GCAGTATTAG ATTTTCATGGG AGCAGCCTCT

FIG.4B

10054841-041600

2251 AATTAGACAA CTTAAGCAAC GTTGCATCGG CTGCTTCTTA TCATTGCTTT
2301 TCCATCTAGA TCAGTTACAG CCATTTGATT CCTTAATTGT TTTTCAAGT
2351 CTTCCAGGTA TTTGTTAGTT TAGCTACTAT GTAACTTTTT CAGGGAATAG
2401 TTTAAGCTTT ATTCATTCAT GCAATACTAA AGAGAAATAA GAATACTGCA
2451 ATTTTGTGCT GGCTTTGAAC AATTACGAAC AATAATGAAG GACAAATGAA
2501 TCCTGAAGGA AGATTTTTTAA AAATGTTTTG TTTCTTCTTA CAAATGGAGA
2551 TTTTTTTGTA CCAGCTTTAC CACTTTTCAG CCATTTATTA ATATGGGAAT
2601 TTAACCTACT CAAGCAATAG TTGAAGGGAA GGTGCATATT ATCACGGATG
2651 CAATTTATGT TGTGTGCCAG TCTGGTCCCA AACATCAATT TCTTAACATG
2701 AGCTCCAGTT TACCTAAATG TTCACTGACA CAAAGGATGA GATTACACCT
2751 ACAGTGACTC TGAGTAGTCA CATATATAAG CACTGCACAT GAGATATAGA
2801 TCCGTAGAAT TGTCAGGAGT GCACCTCTCT ACTTGGGAGG TACAATTGCC
2851 ATATGATTTT TAGCTGCCAT GGTGGTTAGG AATGTGATAC TGCCTGTTTG
2901 CAAAGTCACA GACCTTGCCT CAGAAGGAGC TGTGAGCCAG TATTCATTTA
2951 AGAGAATTCC ACCACACTGG CGGCCCGCGC TTGAT (SEQ ID NO:3)

FIG.4C

14/26

1 GCGGGCCGCCAGTGTGGTGGGAATTCGGCTTGTCACTAGGAGAACATTTGTGTTAATTGCA
-----+-----+-----+-----+-----+-----+ 60
CGCCCGGCGGTCACACCACCTTAAGCCGAACAGTGATCCTCTTGTAACACAATTAACGT

61 CTGTGCTCTGTCAAGGAACTTTGATTTATAGCTGGGGTGCACAAATAATGGTTGCCGGT
-----+-----+-----+-----+-----+-----+ 120
GACACGAGACAGTTCCTTTGAAACTAAATATCGACCCACAGTGTTTATTACCAACGGCCA

121 CGCACATGGATTCCGGTAGAACTTTGCCTTCCTGAATCTTTTTCCCTGCACTACGAGGAAG
-----+-----+-----+-----+-----+-----+ 180
GCGTGTAACCTAAGCCATCTTGAAACGGAAGGACTTAGAAAAAGGGACGTGATGCTCCTTC
M D S V E L C L P E S F S L H Y E E E

181 AGCTTCTCTGCAGAATGTCAAACAAAGATCGACACATTGATTCCAGCTGTTTCGTCCTTCA
-----+-----+-----+-----+-----+-----+ 240
TCGAAGAGACGTCTTACAGTTTGTTTCTAGCTGTGTAACCTAAGGTCGACAAGCAGGAAGT
L L C R M S N K D R H I D S S C S S F I

241 TCAAGACGGAACCTTCCAGCCCAGCCTCCCTGACGGACAGCGTCAACCACCACAGCCCTG
-----+-----+-----+-----+-----+-----+ 300
AGTTCTGCCTTGGAAGGTCGGGTCGGAGGGACTGCCTGTGCGAGTTGGTGGTGTGCGGGAC
K T E P S S P A S L T D S V N H H S P G

301 GTGGCTCTTCAGACGCCAGTGGGAGCTACAGTTCAACCATGAATGGCCATCAGAACGGAC
-----+-----+-----+-----+-----+-----+ 360
CACCGAGAAGTCTGCGGTCAACCCTCGATGTCAAGTTGGTACTTACCGGTAGTCTTGCCTG
G S S D A S G S Y S S T M N G H Q N G L

361 TTGACTCGCCACCTCTCTACCCTTCTGCTCCTATCCTGGGAGGTAGTGGGCCTGTCAGGA
-----+-----+-----+-----+-----+-----+ 420
AACTGAGCGGTGGAGAGATGGGAAGACGAGGATAGGACCCTCCATCACCCGGACAGTCCT
D S P P L Y P S A P I L G G S G P V R K

FIG.5A

10654841.041602

15/26

421 AACTGTATGATGACTGCTCCAGCACCATTGTTGAAGATCCCCAGACCAAGTGTGAATACA 480
 -----+-----+-----+-----+-----+-----+-----+
 TTGACATACTACTGACGAGGTCGTGGTAACAACCTTCTAGGGGTCTGGTTCACACTTATGT
 L Y D D C S S T I V E D P Q T K C E Y M

481 TGCTCAACTCGATGCCCAAGAGACTGTGTTTAGTGTGTGGTGACATCGCTTCTGGGTACC 540
 -----+-----+-----+-----+-----+-----+-----+
 ACGAGTTGAGCTACGGGTTCTCTGACACAAATCACACACCACTGTAGCGAAGACCCATGG
 L N S M P K R L C L V C G D I A S G Y H

541 ACTATGGGGTAGCATCATGTGAAGCCTGCAAGGCATTCTTCAAGAGGACAATTCAAGGCA 600
 -----+-----+-----+-----+-----+-----+-----+
 TGATACCCCATCGTAGTACACTTCGGACGTTCCGTAAGAAGTTCTCCTGTTAAGTTCCGT
Y G V A S C E A C K A F F K R T I Q G N

601 ATATAGAATACAGCTGCCCTGCCACGAATGAATGTGAAATCACAAAGCGCAGACGTAAAT 660
 -----+-----+-----+-----+-----+-----+-----+
 TATATCTTATGTCGACGGGACGGTGCTTACTTACACTTTAGTGTTCGCGTCTGCATTTA
I E Y S C P A T N E C E I T K R R R K S

661 CCTGCCAGGCTTGCCGCTTCATGAAGTGTTTAAAAGTGGGCATGCTGAAAGAAGGGGTGC 720
 -----+-----+-----+-----+-----+-----+-----+
 GGACGGTCCGAACGGCGAAGTACTTCACAAATTTTCACCCGTACGACTTTCTTCCCCACG
C Q A C R F M K C L K V G M L K E G V R

721 GTCTTGACAGAGTACGTGGAGGTCGGCAGAAGTACAAGCGCAGGATAGATGCGGAGAACA 780
 -----+-----+-----+-----+-----+-----+-----+
 CAGAACTGTCTCATGCACCTCCAGCCGTCTTCATGTTTCGCGTCCTATCTACGCCTCTTGT
 L D R V R G G R Q K Y K R R I D A E N S

781 GCCCATACCTGAACCCTCAGCTGGTTCAGCCAGCCAAAAAGCCATATAACAAGATTGTCT 840
 -----+-----+-----+-----+-----+-----+-----+
 CGGGTATGGACTTGGGAGTCGACCAAGTCGGTCGGTTTTTCGGTATATTGTTCTAACAGA
 P Y L N P Q L V Q P A K K P Y N K I V S

FIG.5B

1054841.041602

16/26

841 CACATTTGTTGGTGGCTGAACCGGAGAAGATCTATGCCATGCCTGACCCTACTGTCCCCG 900
 -----+-----+-----+-----+-----+-----+-----+
 GTGTAAACAACCACCGACTTGGCCTCTTCTAGATACGGTACGGACTGGGATGACAGGGGC
 H L L V A E P E K I Y A M P D P T V P D

901 ACAGTGACATCAAAGCCCTCACTACACTGTGTGACTTGGCCGACCGAGAGTTGGTGGTTA 960
 -----+-----+-----+-----+-----+-----+-----+
 TGTCAGTGTAGTTTCGGGAGTGATGTGACACACTGAACCGGCTGGCTCTCAACCACCAAT
 S D I K A L T T L C D L A D R E L V V I

961 TCATTGGATGGGCGAAGCATATTCCAGGCTTCTCCACGCTGTCCCTGGCGGACCAGATGA 1020
 -----+-----+-----+-----+-----+-----+-----+
 AGTAACCTACCCGCTTCGTATAAGGTCCGAAGAGGTGCGACAGGGACCGCCTGGTCTACT
 I G W A K H I P G F S T L S L A D Q M S

1021 GCCTTCTGCAGAGTGCTTGGATGGAAATTTTGATCCTTGGTGTGCGTATACCGGTCTCTTT 1080
 -----+-----+-----+-----+-----+-----+-----+
 CGGAAGACGTCTCACGAACCTACCTTTAAACTAGGAACACAGCATATGGCCAGAGAAA
 L L Q S A W M E I L I L G V V Y R S L S

1081 CATTTGAGGATGAACTTGTCTATGCAGACGATTATATAATGGACGAAGACCAGTCCAAAT 1140
 -----+-----+-----+-----+-----+-----+-----+
 GTAAACTCCTACTTGAACAGATACGTCTGCTAATATATTACCTGCTTCTGGTCAGGTTTA
 F E D E L V Y A D D Y I M D E D Q S K L

1141 TAGCAGGCCTTCTTGATCTAAATAATGCTATCCTGCAGCTGGTAAAGAAATACAAGAGCA 1200
 -----+-----+-----+-----+-----+-----+-----+
 ATCGTCCGGAAGAACTAGATTTATTACGATAGGACGTCGACCATTTCTTTATGTTCTCGT
 A G L L D L N N A I L Q L V K K Y K S M

1201 TGAAGCTGGAAAAAGAAGAATTTGTCACCCTCAAAGCTATAGCTCTTGCTAATTCAGACT 1260
 -----+-----+-----+-----+-----+-----+-----+
 ACTTCGACCTTTTTCTTCTTAAACAGTGGGAGTTTCGATATCGAGAACGATTAAGTCTGA
 K L E K E E F V T L K A I A L A N S D S

FIG.5C

17/26

1261 CCATGCACATAGAAGATGTTGAAGCCGTTTCAGAAGCTTCAGGATGTCTTACATGAAGCGC 1320
-----+-----+-----+-----+-----+-----+
GGTACGTGTATCTTCTACAACCTTCGGCAAGTCTTCGAAGTCCTACAGAATGTACTTCGCG
M H I E D V E A V Q K L Q D V L H E A L

1321 TGCAGGATTATGAAGCTGGCCAGCACATGGAAGACCCTCGTCGAGCTGGCAAGATGCTGA 1380
-----+-----+-----+-----+-----+-----+
ACGTCCTAATACTTCGACCGGTCTGTACCTTCTGGGAGCAGCTCGACCGTTCTACGACT
Q D Y E A G Q H M E D P R R A G K M L M

1381 TGACACTGCCACTCCTGAGGCAGACCTCTACCAAGGCCGTGCAGCATTTCTACAACATCA 1440
-----+-----+-----+-----+-----+-----+
ACTGTGACGGTGAGGACTCCGTCTGGAGATGGTTCCGGCACGTCGTAAAGATGTTGTAGT
T L P L L R Q T S T K A V Q H F Y N I K

1441 AACTAGAAGGCAAAGTCCCAATGCACAACTTTTTTTGGAAATGTTGGAGGCCAAGGTCT 1500
-----+-----+-----+-----+-----+-----+
TTGATCTTCCGTTTCAGGGTTACGTGTTTGAAAAAACCTTTACAACCTCCGGTTCCAGA
L E G K V P M H K L F L E M L E A K V *
(SEQ NO ID:4)

1501 GACTAAAAGCTCCCTGGGCCTTCCCATCCTTCATGTTGAAAAAGGGAAAATAAACCCAAG 1560
-----+-----+-----+-----+-----+-----+
CTGATTTTTCGAGGGACCCGGAAGGGTAGGAAGTACAACCTTTTCCCTTTTATTTGGGTTC

1561 AGTGATGTGAAGAACTTAGAGTTTAGTTAACAAACATCAAAAATCAACAGACTGCACTG 1620
-----+-----+-----+-----+-----+-----+
TCACTACAGCTTCTTTGAATCTCAAATCAATTGTTGTAGTTTTTAGTTGTCTGACGTGAC

1621 ATAATTTAGCAGCAAGACTATGAAGCAGCTTTCAGATTCCTCCATAGGTTTCCTGATGAGT 1680
-----+-----+-----+-----+-----+-----+
TATTAAATCGTCGTTCTGATACTTCGTCGAAAGTCTAAGGAGGTATCCAAGGACTACTCA

FIG.5D

1005441_041602

1681 TCTTTCTACTTTCTCCATCATCTTCTTTCTTTCTTCCCACATTTCTCTTTCTCTTTA
-----+-----+-----+-----+-----+-----+ 1740
AGAAAGATGAAAGAGGTAGTAGAAGAAAGGAGAAAGAAGGGTGTAAAGAGAAAGAGAAAT

1741 TTTTTCTCCTTTTCTTCTTTACCTCCCTTATTTCTTTGCTTCTTTCATTCCTAGTTCC
-----+-----+-----+-----+-----+-----+ 1800
AAAAAAGAGGAAAAGAAGAAAGTGGAGGGAATAAAGAAACGAAGAAAGTAAGGATCAAGG

1801 CATTCTCCTTTATTTTCTTCCCGTCTGCCTGCCTTCTTTCTTTTCTTTACCTACTCTCAT
-----+-----+-----+-----+-----+-----+ 1860
GTAAGAGGAAATAAAAGAAGGGCAGACGGACGGAAGAAAGAAAAGAAATGGATGAGAGTA

1861 TCCTCTCTTTTCTCATCCTTCCCCTTTTTTCTAAATTTGAAATAGCTTTAGTTTAAAAAA
-----+-----+-----+-----+-----+-----+ 1920
AGGAGAGAAAAGAGTAGGAAGGGGAAAAAAGATTTAACCTTTATCGAAATCAAATTTTTT

1921 AAAATCCTCCCTTCCCCCTTTCCCTTTCCCTTTCTTTCCCTTTTCCCTTTCCCTTTCCCT
-----+-----+-----+-----+-----+-----+ 1980
TTTTTAGGAGGGAAGGGGGAAAGGAAAGGGAAAGAAAGGAAAAAGGGAAAGGAAAAGGGA

1981 TTCCTTTCCCTTTCCCTCTTGACCTTCTTTCCATCTTTCTTTTTCTTCCCTTCTGCTGCTGAA
-----+-----+-----+-----+-----+-----+ 2040
AAGGAAAGGAAAGGAGAACTGGAAGAAAGGTAGAAAGAAAAAGAAGGAAGACGACGACTT

FIG.5E

CTTTTAAAAGAGGTCTCTAACTGAAGAGAGATGGAAGCCAGCCCTGCCAAAGGATGGAGA
2041 -----+-----+-----+-----+-----+-----+ 2100
GAAAATTTTCTCCAGAGATTGACTTCTCTCTACCTTCGGTCGGGACGGTTTCCTACCTCT

TCCATAATATGGATGCCAGTGAACCTTATTGTGAACCATACCGTCCCCAATGACTAAGGAA
2101 -----+-----+-----+-----+-----+-----+ 2160
AGGTATTATACCTACGGTCACTTGAATAACACTTGGTATGGCAGGGGTTACTGATTCCTT

TCAAAGAGAGAGAACCAACGTTCTAAAAGTACAGTGCAACATATACAAATTGACTGAGT
2161 -----+-----+-----+-----+-----+-----+ 2220
AGTTTCTCTCTCTTGGTTGCAAGGATTTTCATGTCACGTTGTATATGTTTAACTGACTCA

GCAGTATTAGATTTTCATGGGAGCAGCCTCTAATTAGACAACTTAAGCAACGTTGCATCGG
2221 -----+-----+-----+-----+-----+-----+ 2280
CGTCATAATCTAAAGTACCCTCGTCGGAGATTAATCTGTTGAATTCGTTGCAACGTAGCC

CTGCTTCTTATCATTGCTTTTCCATCTAGATCAGTTACAGCCATTTGATTCCTTAATTGT
2281 -----+-----+-----+-----+-----+-----+ 2340
GACGAAGAATAGTAACGAAAAGGTAGATCTAGTCAATGTCGGTAAACTAAGGAATTAACA

FIG.5F

20/26

2341 TTTTCAAGTCTTCCAGGTATTTGTTAGTTTAGCTACTATGTAACTTTTTCAGGGAATAG 2400
-----+-----+-----+-----+-----+-----+
AAAAAGTTCAGAAGGTCCATAACAATCAAATCGATGATACATTGAAAAAGTCCCTTATC

2401 TTTAAGCTTTATTCATTCATGCAATACTAAAGAGAAATAAGAATACTGCAATTTTGTGCT 2460
-----+-----+-----+-----+-----+-----+
AAATTCGAAATAAGTAAGTACGTTATGATTTCTCTTTATTCTTATGACGTTAAACACGA

2461 GGCTTTGAACAATTACGAACAATAATGAAGGACAAATGAATCCTGAAGGAAGATTTTAA 2520
-----+-----+-----+-----+-----+-----+
CCGAAACTTGTTAATGCTTGTTATTACTTCCTGTTTACTTAGGACTTCCTTCTAAAAATT

2521 AAATGTTTTGTTTCTTCTTACAAATGGAGATTTTTTTGTACCAGCTTTACCACTTTTCAG 2580
-----+-----+-----+-----+-----+-----+
TTTACAAAACAAAGAAGAATGTTTACCTCTAAAAAACATGGTCGAAATGGTGAAAAGTC

2581 CCATTTATTAATATGGGAATTTAACTTACTCAAGCAATAGTTGAAGGGAAGGTGCATATT 2640
-----+-----+-----+-----+-----+-----+
GGTAAATAATTATACCCTTAAATTGAATGAGTTCGTTATCAACTTCCCTTCCACGTATAA

2641 ATCACGGATGCAATTTATGTTGTGTGCCAGTCTGGTCCCAAACATCAATTTCTTAACATG 2700
-----+-----+-----+-----+-----+-----+
TAGTGCCTACGTTAAATACAACACACGGTCAGACCAGGGTTTGTAGTTAAAGAATTGTAC

2701 AGCTCCAGTTTACCTAAATGTTCACTGACACAAAGGATGAGATTACACCTACAGTGACTC 2760
-----+-----+-----+-----+-----+-----+
TCGAGGTCAAATGGATTTACAAGTGACTGTGTTTCTACTCTAATGTGGATGTGCCTGAG

FIG.5G

1006431-041606

21/26

2761 TGAGTAGTCACATATATAAGCACTGCACATGAGATATAGATCCGTAGAATTGTCAGGAGT
-----+-----+-----+-----+-----+-----+ 2820
ACTCATCAGTGTATATATTCGTGACGTGTACTCTATATCTAGGCATCTTAACAGTCCTCA

2821 GCACCTCTCTACTTGGGAGGTACAATTGCCATATGATTTCTAGCTGCCATGGTGGTTAGG
-----+-----+-----+-----+-----+-----+ 2880
CGTGGAGAGATGAACCCTCCATGTTAACGGTATACTAAAGATCGACGGTACCACCAATCC

2881 AATGTGATACTGCCTGTTTGCAAAGTCACAGACCTTGCCTCAGAAGGAGCTGTGAGCCAG
-----+-----+-----+-----+-----+-----+ 2940
TTACACTATGACGGACAAACGTTTCAGTGTCTGGAACGGAGTCTTCCTCGACACTCGGTC

2941 TATTCATTTAAGAGAATTCCACCACACTGGCGGCCCGCGCTTGAT (SEQ ID NO:3)
-----+-----+-----+-----+-----+ 2985
ATAAGTAAATTCTCTTAAGGTGGTGTGACCGCCGGGCGCGAACTA (SEQ ID NO:30)

FIG.5H

105464.041602

1 MDSVELCLPE SFSLHYEEEL LCRMSNKDRH IDSSCSSFIK TEPSSPASLT
51 DSVNHHSPGG SSDASGSYSS TMNGHQNGLD SPPLYPSAPI LGGSGPVRKL
101 YDDCSSTIVE DPQTKCEYML NSMPKRLCLV CGDIASGYHY GVASCEACKA
151 FFKPTIQGNI EYSCPATNEC EITKRRRKSC QACRFMKCLK VGMLKEGVRL
201 DRVRGGRQKY KRRIDAENSP YLNPQLVQPA KKPYNKIVSH LLVAEPEKIY
251 AMPDPTVPDS DIKALTTLCD LADRELVVII GWAKHIPGFS TSLADQMSL
301 LQSAWMEILI LGVVYRSLSF EDELVEYADDY IMDEDQSKLA GLLDLNNAIL
351 QLVKKYKSMK LEKEEFVTLK AIALANSDSM HIEDVEAVQK LQDVLHEALQ
401 DYEAGQHMED PRRAGKMLMT LPLLEQTSTK AVQHFYNIKL EGKVPMHKLF
451 LEMLEAKV* (SEQ ID NO:4)

FIG. 6

10054841.041602

1 GCGGGCCGCC AGTGTGGTGG AATTCGGCTT GTCACTAGGA GAACATTTGT
51 GTTAATTGCA CTGTGCTCTG TCAAGGAAAC TTTGATTTAT AGCTGGGGTG
101 CACAAATAAT GGTTGCCGGT CGCACATGGA TTCGGTAGAA CTTTGCCTTC
151 CTGAATCTTT TTCCCTGCAC TACGAGGAAG AGCTTCTCTG CAGAATGTCA
201 AACAAAGATC GACACATTGA TTCCAGCTGT TCGTCCTTCA TCAAGACGGA
251 ACCTTCCAGC CCAGCCTCCC TGACGGACAG CGTCAACCAC CACAGCCCTG
301 GTGGCTCTTC AGACGCCAGT GGGAGCTACA GTTCAACCAT GAATGGCCAT
351 CAGAACGGAC TTGACTCGCC ACCTCTCTAC CCTTCTGCTC CTATCCTGGG
401 AGGTAGTGGG CCTGTCAGGA AACTGTATGA TGA CTGCTCC AGCACCATTG
451 TTGAAGATCC CCAGACCAAG TGTGAATACA TGCTCAACTC GATGCCCAAG
501 AGACTGTGTT TAGTGTGTGG TGACATCGCT TCTGGGTACC ACTATGGGGT
551 AGCATCATGT GAAGCCTGCA AGGCATTCTT CAAGAGGACA ATTCAAGGCA
601 ATATAGAATA CAGCTGCCCT GCCACGAATG AATGTGAAAT CACAAAGCGC
651 AGACGTAAAT CCTGCCAGGC TTGCCGCTTC ATGAAGTGTT TAAAGTGGG
701 CATGCTGAAA GAAGGGGTGC GTCTTGACAG AGTACGTGGA GGTCGGCAGA
751 AGTACAAGCG CAGGATAGAT GCGGAGAACA GCCCATACCT GAACCCTCAG
801 CTGGTTCAGC CAGCCAAAAA GCCATATAAC AAGATTGTCT CACATTTGTT
851 GGTGGCTGAA CCGGAGAAGA TCTATGCCAT GCCTGACCCT ACTGTCCCCG
901 ACAGTGACAT CAAAGCCCTC ACTACACTGT GTGACTTGGC CGACCGAGAG
951 TTGGTGGTTA TCATTGGATG GGCGAAGCAT ATTCCAGGCT TCTCCACGCT
1001 GTCCCTGGCG GACCAGATGA GCCTTCTGCA GAGTGCTTGG ATGGAAATTT

FIG.7A

1051 TGATCCTTGG TGTCGTATAC CGGTCTCTTT CATTTGAGGA TGAACCTGTC
1101 TATGCAGACG ATTATATAAT GGACGAAGAC CAGTCCAAAT TAGCAGGCCT
1151 TCTTGATCTA AATAATGCTA TCCTGCAGCT GGTAAAGAAA TACAAGAGCA
1201 TGAAGCTGGA AAAAGAAGAA TTTGTCACCC TCAAAGCTAT AGCTCTTGCT
1251 AATTCAGACT CCATGCACAT AGAAGATGTT GAAGCCGTTC AGAAGCTTCA
1301 GGATGTCTTA CATGAAGCGC TGCAGGATTA TGAAGCTGGC CAGCACATGG
1351 AGAAGACCCT CGTCGAGCTG GCAAGATGCT GATGACACTG CCACTCCTGA
1401 GGCAGACCTC TACCAAGGCC GTGCAGCATT TCTACAACAT CAACTAGAA
1451 GGCAAAGTCC CAATGCACAA ACTTTTTTTTG GAAATGTTGG AGGCCAAGGT
1501 CTGACTAAAA GCTCCCTGGG CCTTCCCATC CTTTCATGTTG AAAAAGGGAA
1551 AATAAACCCA AGAGTGATGT CGAAGAACT TAGAGTTTAG TTAACAACAT
1601 CAAAAATCAA CAGACTGCAC TGATAATTTA GCAGCAAGAC TATGAAGCAG
1651 CTTTCAGATT CCTCCATAGG TTCCTGATGA GTTCTTTCTA CTTTCTCCAT
1701 CATCTTCTTT CCTCTTTCTT CCCACATTTT TCTTTCTCTT TATTTTTTCT
1751 CCTTTTCTTC TTTCACCTCC CTTATTTCTT TGCTTCTTTC ATTCCTAGTT
1801 CCCATTCTCC TTTATTTTCT TCCCGTCTGC CTGCCTTCTT TCTTTTCTTT
1851 ACCTACTCTC ATTCCTCTCT TTTCTCATCC TTCCCCTTTT TTCTAAATTT
1901 GAAATAGCTT TAGTTTAAAA AAAAAAATCC TCCCTTCCCC CTTTCCTTTC
1951 CCTTTCTTTC CTTTTTCCCT TTCCTTTTCC CTTTCCTTTC CTTTCCTCTT
2001 GACCTTCTTT CCATCTTTCT TTTTCTTCCT TCTGCTGCTG AACTTTTAAA
2051 AGAGGTCTCT AACTGAAGAG AGATGGAAGC CAGCCCTGCC AAAGGATGGA

FIG.7B

2101 GATCCATAAT ATGGATGCCA GTGAACTTAT TGTGAACCAT ACCGTCCCCA
2151 ATGACTAAGG AATCAAAGAG AGAGAACCAA CGTTCCTAAA AGTACAGTGC
2201 AACATATACA AATTGACTGA GTGCAGTATT AGATTTCATG GGAGCAGCCT
2251 CTAATTAGAC AACTTAAGCA ACGTTGCATC GGCTGCTTCT TATCATTGCT
2301 TTTCCATCTA GATCAGTTAC AGCCATTTGA TTCCTTAATT GTTTTTTCAA
2351 GTCTTCCAGG TATTTGTTAG TTTAGCTACT ATGTAACTTT TTCAGGGAAT
2401 AGTTTAAGCT TTATTCATTC ATGCAATACT AAAGAGAAAT AAGAATACTG
2451 CAATTTTGTG CTGGCTTTGA ACAATTACGA ACAATAATGA AGGACAAATG
2501 AATCCTGAAG GAAGATTTTT AAAAATGTTT TGTTTCTTCT TACAAATGGA
2551 GATTTTTTTG TACCAGCTTT ACCACTTTTC AGCCATTTAT TAATATGGGA
2601 ATTTAACTTA CTCAAGCAAT AGTTGAAGGG AAGGTGCATA TTATCACGGA
2651 TGCAATTTAT GTTGTGTGCC AGTCTGGTCC CAAACATCAA TTTCTTAACA
2701 TGAGCTCCAG TTTACCTAAA TGTTCACTGA CACAAAGGAT GAGATTACAC
2751 CTACAGTGAC TCTGAGTAGT CACATATATA AGCACTGCAC ATGAGATATA
2801 GATCCGTAGA ATTGTCAGGA GTGCACCTCT GTACTTGGGA GGTACAATTG
2851 CCATATGATT TCTAGCTGCC ATGGTGGTTA GGAATGTGAT ACTGCCTGTT
2901 TGCAAAGTCA CAGACCTTGC CTCAGAAGGA GCTGTGAGCC AGTATTCATT
2951 TAAGAGAATT CCACCACACT GGCGGCCCGC GCTTGAT (SEQ ID NO:5)

FIG.7C

1 MDSVELCLPE SFSLHYEEEL LCRMSNKDRH IDSSCSSFIK TEPSSPASLT
51 DSVNHHSPGG SSDASGSYSS TMNGHQGLD SPPLYPSAPI LGGSGPVRKL
101 TDDCSSTIVE DPQTKCEYML NSMPKRLCLV CGDIASGYHY GVASCEACKA
151 FFKRTIQGNI IYSCPATNEC EITKRRRKSC QACRFMKCLK VGMLKEGVRL
201 DRVRGGRQKY KRRIDAENSP YLNPQLVQPA KKPYNKIVSH LLVAEPEKIY
251 AMPDPTVPDS DIKALTTLCD LADRELVVII GWAKHIPGFS TSLADQMSL
301 LQSAWMEILI LGVVYRSLSF EDELVYADDY IMDEDQSKLA GLLDLNNAIL
351 QLVKKYKSMK LEKEEFVTLK AIALANSDSM HIEDVEAVQK LQDVLHEALQ
401 DYEAGQHMEK TLVELARC* (SEQ ID NO:6)

FIG.8